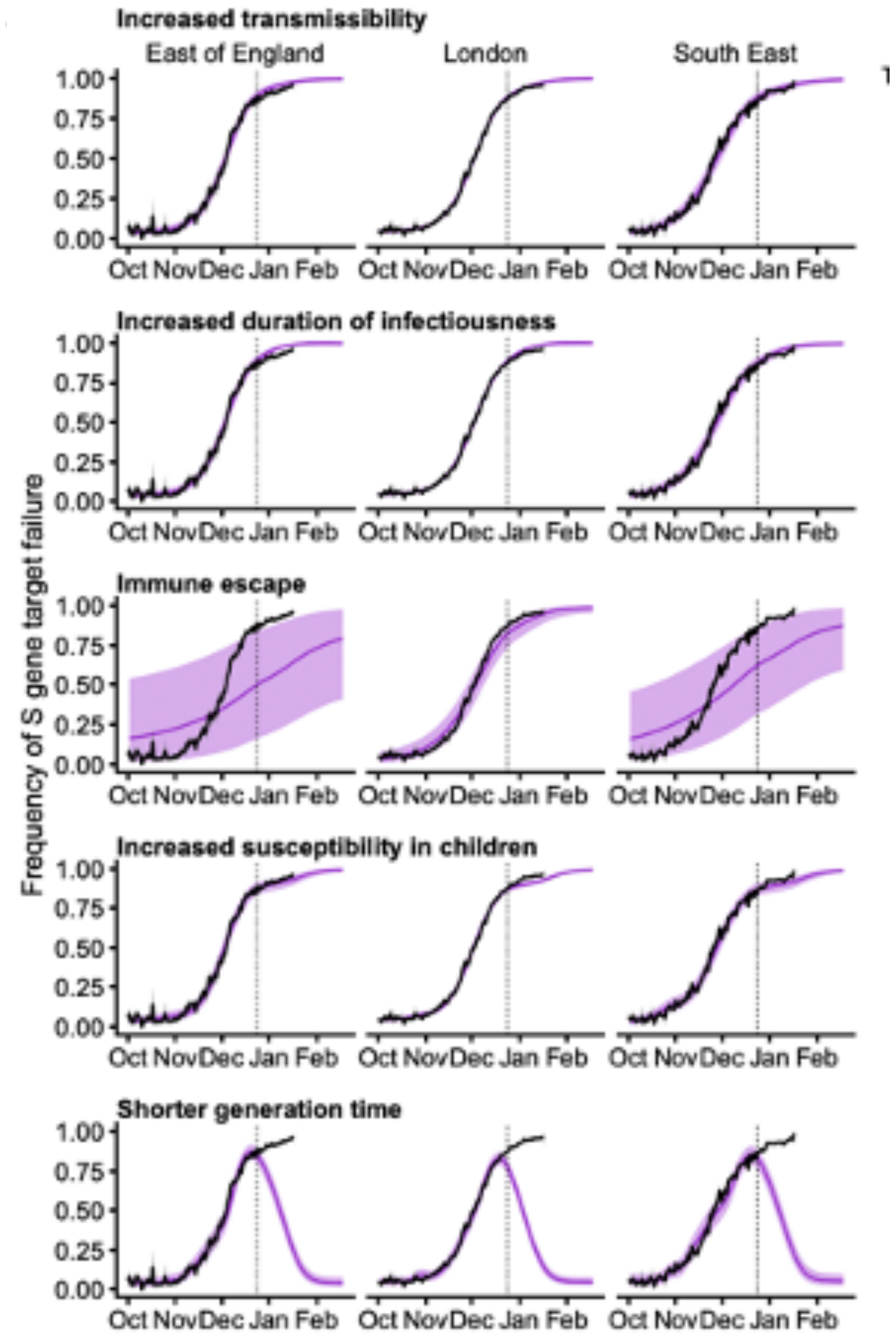
What can we do with the SIR model?

Model prediction
Data

Learn about the pathogen itself

Given the course of the epidemic, what can we infer about the virus?



Davies *et al.* (2021)

Increase β

Reduce γ

Return people from **R** to **S**

Increase β for children only

Reduce β and γ together
(more on this in a few slides!)

$$\frac{dS}{dt} = -\beta IS$$

$$\frac{dI}{dt} = \beta IS - \gamma I$$

$$\frac{dR}{dt} = \gamma I$$

But… where do we get the SIR model's parameters from in the first place?

Option 1: Build up from direct measurements
("forward" model specification)

With enough testing and contact tracing, we can directly measure:

1) the duration of infection (D) and
2) the number of people an infectious person infects (R_0)

Durations are the inverse of rates, so $\boldsymbol{\gamma} = \mathbf{1/D}$**.**

Also, the expected number of infections (R_0) is dictated by a race between the infection rate β and the recovery rate γ.

So, we expect a person to generate $R_0 = \beta/\gamma$ infections.

Given γ, we can therefore calculate $\boldsymbol{\beta} = \mathbf{R_0/}\boldsymbol{\gamma}$**.**

Option 2: Infer from epidemiological data
("reverse" model specification)

Sometimes (often), we don't have the time, money, or resources to make enough direct measurements to estimate everything we'd like to for defining the SIR model.

When this happens, we can try a bunch of different values for β and γ and see which ones fit the data best!

$$S \xrightarrow{\beta I} I \xrightarrow{\gamma} R$$